# User's Manual for the Program Package ECOWEIGHT (C Programs for Calculating Economic Weights in Livestock), Version 5.0.2. Part 3B: Program GFSH for Gene Flow in Sheep, Version 1.0.2

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# Preface

The program GFSH together with the program EWSH2 [6] form the third part of the program package ECOWEIGHT. The program GFSH was written within the framework of the research project MZE0002701404 of the Ministry of Agriculture of the Czech Republic starting in the year 2009. Travelling was funded by the Ministries of Education of the Czech Republic and Slovak Republic (Program KONTAKT, project number MEB 080802 or SK-CZ-0007-07). The technical assistance of Renata Prošková (Prague-Uhříněves), Praha Uříněves, is acknowledged.

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# Chapter 1

# Introduction

The program package ECOWEIGHT is intended for the calculation of economic values of economically important traits in livestock. At the given stage, in its fifth version, two programs for cattle and three programs for sheep are available (see Table 1.1). The two programs for cattle (EWBC and EWDC) are described in the first part of the manual [4]. The second part of the program package is a stand-alone program (EWSH1) for sheep with one lambing per year [5].

Table 1.1: Survey on the program package ECOWEIGHT, version 5.0.2

| Part[a] | Installation Package[b] | Program(s) | Species, remarks |
|---|---|---|---|
| 01 | ECOWEIGHT01_5_0_2.tgz | EWBC | beef cattle |
| | | EWDC | dairy cattle |
| 02 | ECOWEIGHT02_5_0_2.tgz | EWSH1 | sheep, one lambing per year, stand-alone program |
| 03A | ECOWEIGHT03_5_0_2.tgz for both parts 03A and 03B | EWSH2 | sheep, one lambing per year, used in combination with GFSH |
| 03B | | GFSH | sheep, program for gene flow, used in combination with EWSH2 |

[a]There is one manual for each part; its name is ECOWEIGHT[part].pdf where [part] is to be replaced by the two or three digits given in this column.
[b]Replace 'tgz' by 'zip' for Windows.

The third part of the program package which is distributed as one installation package consists of the programs for sheep EWSH2 and GFSH which are documented in two separate manuals. In the present manual, the program GFSH is described which models gene flow in sheep and allows to calculate economic weights for direct and maternal trait components. This program is used in connection with the program EWSH2 [6]. In dependence of the production system, one or more runs of EWSH2 are necessary before GFSH is started.

At the beginning of the present manual, a short description of the general principles of gene transfer is given (Chapter 2). The simplest production system which can be modelled is a pure-bred system with one production level where no distinction is made between nucleus and commercial herds. The calculation of economic weights for direct and maternal trait components for this system is described in Chapter 3. Next a production system with terminal crossing is described where also only one production level is assumed (Chapter 4). In this system, two breeds

are included. A pure-bred system is modelled for sire breed A. In the production system for dam breed B, a part of progeny are pure-bred animals of breed B and another part of progeny are cross-bred animals A×B. That means, the production systems for both breeds are connected via sires from breed A which are crossed to ewes of breed B. Next, relative economic weights are calculated which allow to compare economic weights between traits (Chapter 5).

The next chapters deal with technical details of using the program GFSH. First, information on installing and running the program is given (Chapter 6). The following chapter gives a list of the input files needed for running the program and finally the program output is commented (Chapter 8). The Appendix contains a list of traits with their numbering as it was used in the source code of the program and a list of all variables used in the source code of the program.

# Chapter 2

# General principles of gene flow

Gene flow methods which were developed by Elsen and Moquot [2] and Hill [3] allow studying the flow of genes through a population, which in turn can be used to define the times at which genes are expressed, and by knowing the value of that expression and the number of animals involved, the economic value of that expression can be calculated [1]. At any given time $t$, animals in a population can be divided into a number of different sex and age classes. A gene flow diagram can then be constructed to follow the movement of genes through the population over time.

Time $t$ is given in reproductive cycles (i.e. years in the case of one lambing per year). A vector $\mathbf{m}$ is defined the elements of which define the proportion of genes in each sex and age class. The dimension of the vector is $acm$, the total number of sex and age classes. Assume that the sex and age class $n_sac$ is selected for. Then, at time $t = 0$, all elements of $\mathbf{m}$ with the exception of the $n_sac^{\text{th}}$ element will be zero and the $n_sac^{\text{th}}$ element of $\mathbf{m}$ will be one. Let us write $\mathbf{m^{[t]}}$ for $\mathbf{m}$ at time $t$ and $\mathbf{P}$ for the transmission matrix which is of dimension $acm \times acm$ and the elements $p_{ij}$ of which are the probability that genes from the sex and age class $j$ are transmitted to the sex and age class $i$ during one time unit. Knowing $\mathbf{m^{[0]}}$ (i.e. vector $\mathbf{m}$ at the time 0), $\mathbf{m^{[t]}}$ is calculated as:

$$\mathbf{m^{[t]}} = \mathbf{P m^{[t-1]}} = \mathbf{P^2 m^{[t-2]}} = \ldots = \mathbf{P^t m^{[0]}} \ . \tag{2.1}$$

According to Wolfová and Nitter [7] most traits can be considered to belong to one of two groups in animal breeding. The first group of traits occurs only once in an animal's life (e.g. growth and carcass traits). The second group is realised mostly by females several times in their life (e.g. lactation and fertility traits, but also wool traits). For simplicity we will designate the first group as direct traits and the second group as maternal traits having in mind that the second group of traits may be exceptionally also expressed in males (wool traits). Some traits (growth of lambs until weaning or conception rate) are composite traits with a direct and a maternal genetic component, the direct component realized once by the offspring and the maternal component realized several times during the female's life.

For the calculation of the number of discounted expressions, we need so-called realization vectors, $\mathbf{h_d}$ and $\mathbf{h_m}$, for direct and maternal effects, respectively. A realization vector describes the extend of the expression of a trait in the individual sex and age classes. Therefore, both realization vectors are of dimension $acm$. Examples for realization vectors are given in the following chapters.

Out of the analyzed traits (see Appendix A), the following ones are considered to be direct traits: growth rates in artificial rearing, in fattening and in rearing of breeding animals, survival rates in artificial rearing and all carcass traits, (traits

4 to 7, 9 to 19 and 25). On the other hand, mature weight, milk yield, fat and protein content or yield, somatic cell count, average litter size, wool production and productive life of ewes are considered to be maternal traits (traits 8, 22 and 26 to 35). Mature weight is considered as "maternal trait" because there are maintenance costs in each reproductive cycle. Wool is repeatedly sheared. Productive lifetime may be understood as a result of successive surviving in the individual reproductive cycles.

Several traits have direct and maternal components: birth weight, weaning weight, growth rate from birth till weaning, survival rate of lambs at birth and until weaning and conception rate (traits 1 to 3, 20, 21, 23 and 24). The direct component of growth traits till weaning expresses the genetic potential of lambs for growth, the maternal component expresses the genetic potential of the dam for milk available to lambs. The direct effect of the lamb survival rate expresses the health status of the lambs, the maternal effect is determined by the mothering ability of a ewe[1].

[1] Maternal components of growth traits and survival rates till weaning will therefore be expressed both on pure-bred and on cross-bred progeny.

# Chapter 3

# Production system 1: Pure-bred system with one production level

In this system, the population of sheep is not distinguished in nucleus and commercial herds. The system is similar as in cattle, where the dams of sires are selected from the whole population (see Fig. 3.1). Only one breed is considered in this production system and the capital letter "A" is used to designate this breed; this letter is used at the end of several variables to make clear that these variables refer to breed A.

The number of age classes for sires ($acsA$)[1] is calculated as

$$acsA = \text{int}\left(\frac{ageR11A}{365}\right) + RRA \tag{3.1}$$

and the number of age classes for dams ($acdA$) is

$$acdA = \text{int}\left(\frac{ageE1A}{365}\right) + LLA\ . \tag{3.2}$$

[1] All variables are explained in Appendix B

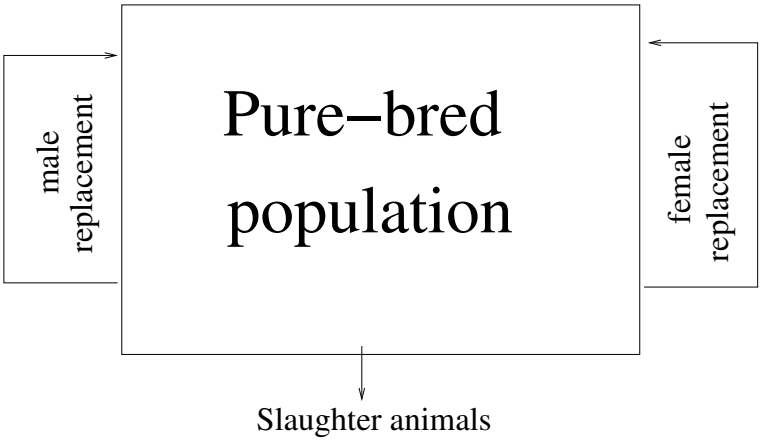


Figure 3.1: Pure-bred system with one production level

**Algorithm 3.1** Structure of matrix **P**. The symbol "x" characterizes elements which can be different from zero (The values of "x" are in the range from 0 to 0.5).

$$
\mathbf{P} = \begin{array}{c}
\begin{array}{cccccc|cccccc|c}
\multicolumn{6}{c|}{\text{Sires}} & \multicolumn{6}{c|}{\text{Dams}} & \text{Slaughter animals} \\
\end{array} \\
\left[\begin{array}{cccccc|cccccc|c}
\text{x} & \text{x} & \text{x} & \cdots & \text{x} & \text{x} & \text{x} & \text{x} & \text{x} & \cdots & \text{x} & \text{x} & 0 \\
1 & 0 & 0 & \cdots & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 & 0 \\
0 & 1 & 0 & \cdots & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 & 0 \\
0 & 0 & 1 & \cdots & 0 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 & 0 \\
0 & 0 & 0 & \ddots & 0 & 0 & 0 & 0 & 0 & \ddots & 0 & 0 & 0 \\
0 & 0 & 0 & \cdots & 1 & 0 & 0 & 0 & 0 & \cdots & 0 & 0 & 0 \\
\hline
\text{x} & \text{x} & \text{x} & \cdots & \text{x} & \text{x} & \text{x} & \text{x} & \text{x} & \cdots & \text{x} & \text{x} & 0 \\
0 & 0 & 0 & \cdots & 0 & 0 & 1 & 0 & 0 & \cdots & 0 & 0 & 0 \\
0 & 0 & 0 & \cdots & 0 & 0 & 0 & 1 & 0 & \cdots & 0 & 0 & 0 \\
0 & 0 & 0 & \cdots & 0 & 0 & 0 & 0 & 1 & \cdots & 0 & 0 & 0 \\
0 & 0 & 0 & \ddots & 0 & 0 & 0 & 0 & 0 & \ddots & 0 & 0 & 0 \\
0 & 0 & 0 & \cdots & 0 & 0 & 0 & 0 & 0 & \cdots & 1 & 0 & 0 \\
\hline
\text{x} & \text{x} & \text{x} & \cdots & \text{x} & \text{x} & \text{x} & \text{x} & \text{x} & \cdots & \text{x} & \text{x} & 0
\end{array}\right]
\end{array}
\begin{array}{l}
\\
\text{Sires} \\
\\
\\
\\
\\
\\
\text{Dams} \\
\\
\\
\\
\\
\\
\text{Slaughter animals}
\end{array}
$$

The dimension of the transmission matrix **P** for gene flow ($acm$) is then

$$acm = acsA + acdA + 1 \ . \tag{3.3}$$

## 3.1 Calculation of the elements of the transmission matrix P

Matrix **P** has a block structure containing 3×3 blocks (see Algorithm 3.1). Therefore we can write matrix **P** in the form:

$$\mathbf{P} = \begin{bmatrix} \mathbf{P_{11}} & \mathbf{P_{12}} & \mathbf{P_{13}} \\ \mathbf{P_{21}} & \mathbf{P_{22}} & \mathbf{P_{23}} \\ \mathbf{P_{31}} & \mathbf{P_{32}} & \mathbf{P_{33}} \end{bmatrix} \tag{3.4}$$

The elements $P[i][j]$ of **P** are the proportions of genes in the sex and age class $i$ at time $t$ which come from the sex and age class $j$ at time $t-1$. The sum of all elements $P[i][j]$ within each row is 1. The sum of all elements $P[i][j]$ within each row belonging to the same sex is 0.5 if there are non-zero elements for both sexes in this row. This is the case when vertically new blocks start (see Algorithm 3.1). For calculating the elements $P[i][j]$ $(i, j = 1, \ldots, acm)$ of **P**, first all elements are set to zero. Then the non-zero elements are inserted as given below.

### 3.1.1 Submatrix $\mathbf{P_{11}}$

Submatrix $\mathbf{P_{11}}$ is the "sires-to-sires" part of the transmission matrix and is of dimension $acsA \times acsA$. The elements of the first row may be read in from input file INPUTGFS02.TXT if the sires for the production of rams are selected from certain age classes. If there is no selection among sires of rams, the elements in the first row are calculated as follows:

$$P[1][acsA - RRA + i] = 0.5 \times l4RA[i] \qquad \text{where} \qquad i = 1, \ldots, RRA \ . \tag{3.5}$$

The further elements different from zero are:

$$P[i+1][i] = 1 \qquad \text{for} \qquad i = 1, \ldots, acsA - 1 \ . \tag{3.6}$$

The diagonal of elements 1 describes aging of animals of the given group.

### 3.1.2 Submatrix $\mathbf{P_{12}}$

The submatrix $\mathbf{P_{12}}$ is the "dams-to-sires" part of the transmission matrix and is of dimension $acsA \times acdA$. The elements of the first row may be read in from input file INPUTGFS02.TXT if the dams for the production of rams are selected from certain age classes. If there is no selection among dams of rams, the elements in the first row are calculated as follows:

$$P[1][acsA + acdA - LLA + i] = 0.5 \times l4EA[i] \qquad \text{where} \qquad i = 1, \ldots, LLA \ . \tag{3.7}$$

These are the only elements different from zero in this submatrix.

### 3.1.3 Submatrix $\mathbf{P_{21}}$

The submatrix $\mathbf{P_{21}}$ is the "sires-to-dams" part of the transmission matrix and is of dimension $acdA \times acsA$. The elements of its first row are:

$$P[acsA+1][acsA-RRA+i] = 0.5 \times l4RA[i] \qquad \text{where} \qquad i = 1, \ldots, RRA \ . \tag{3.8}$$

These are the only elements different from zero in this submatrix.

### 3.1.4 Submatrix $\mathbf{P_{22}}$

The submatrix $\mathbf{P_{22}}$ is the "dams-to-dams" part of the transmission matrix and is of dimension $acdA \times acdA$. The elements of its first row are:

$$P[acsA+1][acsA+acdA-LLA+i] = 0.5 \times l4EA[i] \qquad \text{where} \qquad i = 1, \ldots, LLA \ . \tag{3.9}$$

The further elements different from zero are:

$$P[acsA + i + 1][acsA + i] = 1 \qquad \text{for} \qquad i = 1, \ldots, acdA - 1 \ . \tag{3.10}$$

The diagonal of elements 1 again describes aging of animals of the given group.

### 3.1.5 Submatrix $\mathbf{P_{31}}$

The submatrix $\mathbf{P_{31}}$ is the "sires-to-slaughter animals" part of the transmission matrix and is of dimension $1 \times acsA$. The elements of its only row are the same as the elements in the first row of submatrix $\mathbf{P_{21}}$:

$$P[acm][acsA - RRA + i] = 0.5 \times l4RA[i] \qquad \text{where} \qquad i = 1, \ldots, RRA \ . \tag{3.11}$$

### 3.1.6 Submatrix $\mathbf{P_{32}}$

The submatrix $\mathbf{P_{32}}$ is the "dams-to-slaughter animals" part of the transmission matrix and is of dimension $1 \times acdA$. The elements of its only row are the same as the elements in the first row of submatrix $\mathbf{P_{31}}$:

$$P[acm][acsA + acdA - LLA + i] = 0.5 \times l4EA[i] \qquad \text{where} \qquad i = 1, \ldots, LLA \ . \tag{3.12}$$

### 3.1.7 Submatrices $\mathbf{P_{13}}$, $\mathbf{P_{23}}$ and $\mathbf{P_{33}}$

The matrices $\mathbf{P_{13}}$, $\mathbf{P_{23}}$ and $\mathbf{P_{33}}$ are the "slaughter animals to sires", "slaughter animals to dams" and "slaughter animals to slaughter animals" parts, respectively, of the transmission matrix. The dimension of these matrices is $1 \times acsA$, $1 \times acdA$ and $1 \times 1$. As no genes are transmitted from slaughter animals, all elements of these submatrices are zero.

## 3.2 Calculation of vectors m ($m_gf[*]$[2] in the program), $\mathbf{h_d}$ and $\mathbf{h_m}$

Given is $n_sac$, the number of the sex and age class the selection is carried out for. To get $\mathbf{m^{[0]}}$ from equation (2.1), all elements of the vector $m_gf[*]$ are set to zero and $m_gf[n_sac] = 1$. Then equation (2.1) is applied to calculate $\mathbf{m^{[t]}}$. The expression $\sum_{t=1}^{l_inv} \mathbf{m^{[t]}}(1+u)^{-t}$ is calculated as vector $m_sum[*]$ in the program.

The notations $h_d[*]$ and $h_m[*]$ are used in the program for $\mathbf{h_d}$ and $\mathbf{h_m}$. The last element of the vector $h_d[*]$ is one:

$$h_d[acm] = 1 \tag{3.13}$$

and all remaining elements of the vector are zero. The first $acsA$ elements and the last element of $h_m[*]$ are zero. Furthermore the elements $acsA + 1$ to $acsA + acdA - LLA$ are zero if $acdA > LLA$. The remaining elements are:

$$h_m[acsA + acdA - LLA + i] = l4EA[i] \qquad \text{for} \qquad i = 1, \ldots, LLA\ . \tag{3.14}$$

## 3.3 Calculation of economic weights

The economic weights for direct effects ($ew_d[i]$) and for maternal effects ($ew_m[i]$) of trait $i$ are calculated as follows:

$$\begin{aligned} ew_d[i] &= evp[i][1] \times \sum_{i=1}^{acm} h_d[i] \times m_sum[i] \quad \text{if } tt[i] = 0 \text{ or } tt[i] = 2 \\ ew_m[i] &= evp[i][1] \times \sum_{i=1}^{acm} h_m[i] \times m_sum[i] \quad \text{if } tt[i] = 1 \text{ or } tt[i] = 2\ . \end{aligned} \tag{3.15}$$

[2] In most cases the same symbols for variables are used in the manual and in the program written in C. For differentiating between a vector or a matrix (generally an array) and its elements, we use an index $i, j, k$ etc. for an element of the array and use the symbol '*' instead of an index to refer to the array as such.

# Chapter 4

# Production system 2: System with terminal crossing and one production level only

In this production system, specialized sire and dam breeds are assumed. Sire and dam breed flocks are assumed to be self-replacing producing both males and females for own replacement (selling and purchasing of breeding animals between farms within each breed is not taken into account in the profit function for the calculation of economic values). Sire breed flocks produce also sires for terminal crossing in the dam breed flocks (see Figure 4.1).

The number of age classes for sires of breed A used for pure-breeding ($acsA$) and the number of age classes for dams of breed A ($acdA$) are calculated according to equations (3.1) and (3.2), respectively. The age classes for sires of breed B ($acsB$) and the number of age classes for dams of breed B ($acdB$) are calculated in the same way as the corresponding variables for breed A (replace "A" by "B" in equations (3.1) and (3.2)). The number of age classes for sires of breed A used for cross-breeding with ewes of breed B ($acsAB$) is[1]:

$$acsAB = \text{int}\left(\frac{ageR12A}{365}\right) + RRB \ . \tag{4.1}$$

The total number of sex and age classes which is identical with the dimension

[1] The same age structure and the same number of breeding cycles is assumed for rams of breeds A and B in the flock of breed B.

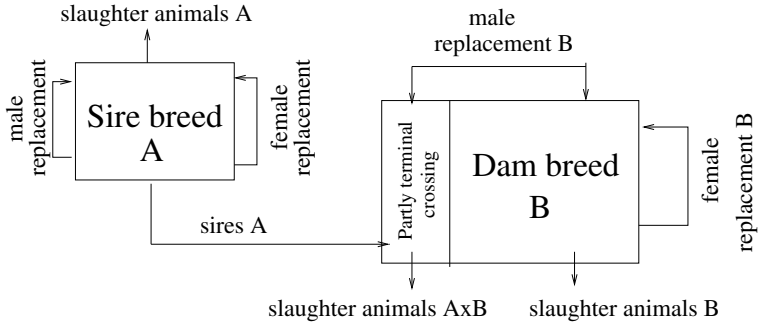


Figure 4.1: System with terminal crossing on one production level

of the transmission matrix $\mathbf{P}$ for gene flow ($acm$) is then

$$acm = acsA + acdA + acsAB + acsB + acdB + 3\ . \tag{4.2}$$

## 4.1 Calculation of the elements of the transmission matrix P

Matrix $\mathbf{P}$ has a block structure containing 8×8 blocks and can be therefore written as:

$$\mathbf{P} = \begin{bmatrix} \mathbf{P_{11}} & \mathbf{P_{12}} & \cdots & \mathbf{P_{18}} \\ \mathbf{P_{21}} & \mathbf{P_{22}} & \cdots & \mathbf{P_{28}} \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{P_{81}} & \mathbf{P_{82}} & \cdots & \mathbf{P_{88}} \end{bmatrix} \tag{4.3}$$

This structure is the consequence of the following 8 groups of sex and age classes (in parentheses the number of classes is given):

- Age classes for sires of breed A used for pure-breeding ($acsA$)
- Age classes for dams of breed A ($acdA$)
- Age classes for sires of breed A used for crossing with ewes of breed B ($acsAB$)
- Age classes for sires of breed B ($acsB$)
- Age classes for dams of breed B ($acdB$)
- Age class for slaughter animals of breed A (1)
- Age class for slaughter animals of breed B (1)
- Age class for slaughter animal A×B (1)

All submatrices of $\mathbf{P}$ with non-zero elements have one of the following structures $\mathbf{S_1}$ to $\mathbf{S_4}$ (the symbol "x" characterizes elements which may be different from zero):

$$\mathbf{S_1} = \begin{bmatrix} \mathrm{x} & \mathrm{x} & \mathrm{x} & \cdots & \mathrm{x} & \mathrm{x} \\ 1 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 1 & 0 & \cdots & 0 & 0 \\ 0 & 0 & 1 & \cdots & 0 & 0 \\ 0 & 0 & 0 & \ddots & 0 & 0 \\ 0 & 0 & 0 & \cdots & 1 & 0 \end{bmatrix} \tag{4.4}$$

$$\mathbf{S_2} = \begin{bmatrix} \mathrm{x} & \mathrm{x} & \mathrm{x} & \cdots & \mathrm{x} & \mathrm{x} \\ 0 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 0 & 0 & \ddots & 0 & 0 \\ 0 & 0 & 0 & \cdots & 0 & 0 \end{bmatrix} \tag{4.5}$$

$$\mathbf{S_3} = \begin{bmatrix} \mathrm{x} & \mathrm{x} & \mathrm{x} & \cdots & \mathrm{x} & \mathrm{x} \end{bmatrix} \tag{4.6}$$

$$\mathbf{S_4} = \begin{bmatrix} 0 & 0 & 0 & \cdots & 0 & 0 \\ 1 & 0 & 0 & \cdots & 0 & 0 \\ 0 & 1 & 0 & \cdots & 0 & 0 \\ 0 & 0 & 1 & \cdots & 0 & 0 \\ 0 & 0 & 0 & \ddots & 0 & 0 \\ 0 & 0 & 0 & \cdots & 1 & 0 \end{bmatrix} \tag{4.7}$$

### 4.1.1 Submatrices $\mathbf{P_{11}}$, $\mathbf{P_{12}}$, $\mathbf{P_{21}}$ and $\mathbf{P_{22}}$

The elements of submatrices $\mathbf{P_{11}}$, $\mathbf{P_{12}}$, $\mathbf{P_{21}}$ and $\mathbf{P_{22}}$ are calculated in the same way as in production system 1 (subsections 3.1.1 to 3.1.4, equations 3.5 to 3.10) so that submatrices $\mathbf{P_{11}}$ and $\mathbf{P_{22}}$ are of the structure $\mathbf{S_1}$ and submatrices $\mathbf{P_{12}}$ and $\mathbf{P_{21}}$ are of the structure $\mathbf{S_2}$. The elements of the first rows of submatrices $\mathbf{P_{11}}$ and $\mathbf{P_{12}}$ may be read in from input file INPUTGFS03.TXT.

### 4.1.2 Submatrices $\mathbf{P_{31}}$ and $\mathbf{P_{32}}$

Submatrices $\mathbf{P_{31}}$ and $\mathbf{P_{32}}$ are of the structure $\mathbf{S_2}$. $\mathbf{P_{31}}$ represents the gene flow from sires of breed A used for pure-breeding to sires of breed A used for cross-breeding and $\mathbf{P_{32}}$ represents the gene flow from dams of breed A to sires of breed A used for cross-breeding. $\mathbf{P_{31}}$ and $\mathbf{P_{32}}$ are of dimension $acsAB \times acsA$ and $acsAB \times acdA$, respectively. The non-zero elements of $\mathbf{P_{31}}$ are:

$$P[acsA + acdA + 1][i] = P[1][i] \quad \text{for} \quad i = 1, \ldots, acsA \ , \tag{4.8}$$

i.e. they are the same as the elements in the first row of $\mathbf{P_{11}}$. The non-zero elements of $\mathbf{P_{32}}$ are:

$$P[acsA + acdA + 1][acsA + i] = P[1][acsA + i] \quad \text{for} \quad i = 1, \ldots, acdA \ , \tag{4.9}$$

i.e. they are the same as the elements in the first row of $\mathbf{P_{12}}$.

### 4.1.3 Submatrix $\mathbf{P_{33}}$

$\mathbf{P_{33}}$ is the sires to sires matrix for sires of breed A used for cross-breeding with dams of breed B. It is of type $\mathbf{S_4}$. Consequently, its non-zero elements are:

$$P[acsA + acdA + i + 1][acsA + acdA + i] = 1 \quad \text{for} \quad i = 1, \ldots, acsAB - 1 \ . \tag{4.10}$$

### 4.1.4 Submatrices $\mathbf{P_{44}}$ and $\mathbf{P_{55}}$

$\mathbf{P_{44}}$ is the sires to sires matrix for breed B and $\mathbf{P_{55}}$ is the dams to dams matrix for breed B. Both matrices are of type $\mathbf{S_1}$. The elements of the first row of $\mathbf{P_{44}}$ may be read in from input file INPUTGFS03.TXT if the sires of breed B for the production of rams are selected from certain age classes. Otherwise the elements of the first row of $\mathbf{P_{44}}$ are calculated as follows:

$$\begin{aligned} P[acsA + acdA + acsAB + 1][acsA + acdA + acsAB + acsB - RRB + i] \quad = \\ 0.5 \times l4RB[i] \quad \text{for} \quad i = 1, \ldots, RRB \ . \end{aligned} \tag{4.11}$$

The remaining non-zero elements of $\mathbf{P_{44}}$ are:

$$P[acsA+acdA+acsAB+i+1][acsA+acdA+acsAB+i] = 1 \text{ for } i = 1, \ldots, acsB-1 \ . \tag{4.12}$$

The elements of the first row of $\mathbf{P_{55}}$ are:

$$P[j][k] = 0.5 \times l4EB[i] \quad \text{for} \quad i = 1, \ldots, LLB \tag{4.13}$$

where

$$j = acsA + acdA + acsAB + acsB + 1 \quad \text{and}$$
$$k = acsA + acdA + acsAB + acsB + acdB - LLB + i \ .$$

The further non-zero elements of $\mathbf{P_{55}}$ are:

$$P[acm - acdB - 2 + i][acm - acdB - 3 + i] = 1 \quad \text{for} \quad i = 1, \ldots, acdB - 1 \ . \tag{4.14}$$

### 4.1.5 Submatrices $\mathbf{P_{45}}$ and $\mathbf{P_{54}}$

$\mathbf{P_{45}}$ is the dams to sires matrix for breed B and $\mathbf{P_{54}}$ is the sires to dams matrix for breed B. Both matrices are of type $\mathbf{S_2}$. The elements of the first row of $\mathbf{P_{45}}$ may be read in from input file INPUTGFS03.TXT if the dams for the production of rams are selected from certain age classes. Otherwise the non-zero elements of matrix $\mathbf{P_{45}}$ are calculated in the program:

$$P[j][k] = 0.5 \times l4EB[i] \quad \text{for} \quad i = 1, \ldots, LLB \tag{4.15}$$

where

$$j = acsA + acdA + acsAB + 1 \quad \text{and}$$
$$k = acsA + acdA + acsAB + acsB + acdB - LLB + i \ .$$

The elements of the first row of $\mathbf{P_{54}}$ are calculated as:

$$P[j][k] = 0.5 \times l4RB[i] \quad \text{for} \quad i = 1, \ldots, RRB \tag{4.16}$$

where

$$j = acsA + acdA + acsAB + acsB + 1 \quad \text{and}$$
$$k = acsA + acdA + acsAB + acsB - RRB + i \ .$$

### 4.1.6 Submatrices $\mathbf{P_{61}}$ and $\mathbf{P_{62}}$

$\mathbf{P_{61}}$ is the sires A to slaughter animals A matrix and $\mathbf{P_{62}}$ is the dams A to slaughter animals A matrix. Both matrices are of type $\mathbf{S_3}$. The elements of matrix $\mathbf{P_{61}}$ are:

$$P[acm-2][acsA - RRA + i] = 0.5 \times l4RA[i] \quad \text{for} \quad i = 1, \ldots, RRA \tag{4.17}$$

and the elements of matrix $\mathbf{P_{62}}$ are:

$$P[acm-2][acsA+acdA-LLA+i] = 0.5 \times l4EA[i] \quad \text{for} \quad i = 1, \ldots, LLA \ . \tag{4.18}$$

That means the elements of $\mathbf{P_{61}}$ are the same as the elements in the first row of $\mathbf{P_{21}}$ and the elements of $\mathbf{P_{62}}$ are the same as the elements in the first row of $\mathbf{P_{22}}$.

### 4.1.7 Submatrices $\mathbf{P_{74}}$ and $\mathbf{P_{75}}$

$\mathbf{P_{74}}$ is the sires B to slaughter animals B matrix and $\mathbf{P_{75}}$ is the dams B to slaughter animals B matrix. Both matrices are of type $\mathbf{S_3}$. The elements of matrix $\mathbf{P_{74}}$ are:

$$P[acm-1][acsA + acdA + acsAB + acsB - RRB + i] \quad = \quad 0.5 \times l4RB[i] \quad \text{for} \quad i = 1, \ldots, RRB \tag{4.19}$$

and the elements of matrix $\mathbf{P_{75}}$ are:

$$P[j][k] = 0.5 \times l4EB[i] \times \frac{1 - pcrossE[i-1]}{\sum_{l=1}^{LLB}(1 - pcrossE[l-1])} \quad \text{for} \quad i = 1, \ldots, LLB \tag{4.20}$$

where

$$j = acm - 1 \quad \text{and}$$
$$k = acsA + acdA + acsAB + acsB + acdB - LLB + i \ .$$

The elements of $\mathbf{P_{74}}$ are the same as the elements in the first row of $\mathbf{P_{54}}$.

### 4.1.8 Submatrix $\mathbf{P_{83}}$

$\mathbf{P_{83}}$ is the sires A to cross-bred slaughter animals matrix. It is of type $\mathbf{S_3}$. Its elements are:

$$P[acm][acsA + acdA + acsAB - RRB + i] = 0.5 \times l4RB[i] \quad \text{for} \quad i = 1, \ldots, RRB \ . \tag{4.21}$$

### 4.1.9 Submatrix $\mathbf{P_{85}}$

$\mathbf{P_{85}}$ is the dams B to cross-bred slaughter animals matrix. It is of type $\mathbf{S_3}$. Its elements are:

$$P[j][k] = 0.5 \times l4EB[i] \times \frac{pcrossE[i-1]}{\sum_{l=1}^{LLB} pcrossE[l-1]} \quad \text{for} \quad i = 1, \ldots, LLB \tag{4.22}$$

where

$$j = acm \quad \text{and}$$
$$k = acsA + acdA + acsAB + acsB + acdB - LLB + i \ .$$

## 4.2 Vectors m ($m_gf[*]$ in the program), $\mathbf{h_d}$ and $\mathbf{h_m}$

Vectors $m_gf[*]$ and $m_sum[*]$ are calculated in the same way as in production system 1 (see section 3.2 on page 13). They are of dimension $acm$ and can be subdivided into 8 blocks in the same way as matrix $\mathbf{P}$.

Also vectors $h_d[*]$ and $h_m[*]$ are of dimension $acm$ and have 8 blocks. In vector $h_d[*]$, only the elements referring to slaughter animals are different from zero:

$$h_d[acm-2] = pdA, \quad h_d[acm-1] = h_d[acm] = pdB \tag{4.23}$$

In the vector for maternal effects, $h_m[*]$, non-zero elements are in the blocks "dams A" and "dams B":

$$\begin{aligned} h_m[acsA + acdA - LLA + i] &= l4EA[i] \times pdA \quad \text{for} \quad i = 1, \ldots, LLA \\ h_m[acm - 3 - LLB + i] &= l4EB[i] \times pdB \quad \text{for} \quad i = 1, \ldots, LLB \end{aligned} \tag{4.24}$$

The elements of the vector $\mathbf{h_m}$ sum to 1.

## 4.3 Calculation of economic weights

By multiplying the vectors $h_d[*]$ and $h_m[*]$ with the marginal economic values of each trait, the matrices $he_d[*][*]$ and $he_m[*][*]$ are calculated. The first index of the matrices refers to the number of the trait and the second index refers to the sex and age class. First, all elements of the matrices $he_d[*][*]$ and $he_m[*][*]$ are set zero. The non-zero elements of $he_d[*][*]$ are calculated as follows (for $i = 1, \ldots, NT-1$):

$$\begin{aligned} he_d[i][acm-2] &= h_d[acm-2] \times evpA[i][1] \\ he_d[i][acm-1] &= h_d[acm-1] \times evpB[i][1] \\ he_d[i][acm] &= h_d[acm] \times evpB[i][2] \end{aligned} \tag{4.25}$$

Table 4.1: Values of $tt[i]$

| Number of the trait[a] ($i$) | Value of $tt[i]$ |
|---|---|
| 4 to 7, 9 to 19, 20, 25 | 0 |
| 8, 22, 26 to 35 | 1 |
| 1 to 3, 21, 23, 24 | 2 |

[a]See Appendix A for numbering traits

The non-zero elements of $he_m[*][*]$ are (for $i = 1, \ldots, NT - 1$):

$$\begin{aligned} he_m[i][j] &= h_m[j] \times evpA[i][1] \quad \text{for} \quad j = acsA + 1, \ldots, acsA + acdA \\ he_m[i][j] &= h_m[j] \times (evpB[i][1] + evpB[i][2]) \\ &\quad \text{for} \quad j = acm - acdB - 2, \ldots, acm - 3 \end{aligned} \tag{4.26}$$

The economic weights for the direct and the maternal components of trait $i$, $ew_d[i]$ and $ew_m[i]$, are calculated as follows:

$$\begin{aligned} ew_d[i] &= \sum_{j=1}^{acm} he_d[i][j] \times m_sum[j] \quad \text{if } tt[i] = 0 \text{ or } tt[i] = 2 \\ ew_m[i] &= \sum_{j=1}^{acm} he_m[i][j] \times m_sum[j] \quad \text{if } tt[i] = 1 \text{ or } tt[i] = 2 \end{aligned} \tag{4.27}$$

where

$$tt[i] = \begin{cases} 0 & \text{if there is only a direct component of trait } i \\ 1 & \text{if there is only a maternal component of trait } i \\ 2 & \text{if there are both a direct and a maternal component of trait } i \end{cases}$$

The values of $tt[i]$ are fixed in the program (see Table 4.1). These economic weights are valid for the sex and age class of animals which is determined by the variable $n_sac$. The economic weight of trait $i$ or component of trait $i$ represents the present value (in monetary units) of one unit genetic superiority of the selected group of animals in this trait transmitted in the evaluated production (breeding) system during the defined investment period per ewe in this production system. If the economic weights are calculated for breed A they can be easily converted to be per ewe of breed A by dividing the weights calculated by equation (4.27) by the proportion of ewes of breed A in the production system ($pdA$). Similarly, the economic weights per ewe of breed B may be calculated by dividing the weights from equation (4.27) by the proportion of ewes of breed B in the production system ($pdB$).

# Chapter 5

# Relative economic weights

The economic weights of the individual traits as they are calculated in sections 3.3 and 4.3 cannot be compared among each other as they have different units. One way to make the economic weights comparable is to refer them to the genetic standard deviation of the trait. These so-called standardized economic weights for the direct and the maternal trait components ($ewst_d[i]$ and $ewst_m[i]$) are calculated as:

$$\begin{aligned} ewst_d[i] &= ew_d[i] \times gstd_d[i] \\ ewst_m[i] &= ew_m[i] \times gstd_m[i] \end{aligned} \tag{5.1}$$

where $gstd_d[i]$ and $gstd_m[i]$ are the genetic standard deviations for the direct and maternal components of trait $i$ ($i = 1, \ldots, NT-1$).The standardized economic weights are given in monetary units per standard deviation of the trait component and per ewe in the whole production system.

As the standardized economic weights have the same units for all traits, they can be expressed as percentage of the sum of all standardized economic weights. When calculating the sum, care must be taken of not including the same trait twice. Therefore, in input file INPUTGFS05.TXT (see Subsection 7.2.6) you must choose always one trait definition from two alternatives for six paires of definitions describing always the same trait in different ways.

As both positive and negative values occur it is useful to calculate the sum from the absolute values of the economic weights. It may be useful to calculate this sum for the economic weights of the direct components of the traits ($ewsum_d$), for the economic weights of the maternal components of the traits ($ewsum_m$) and for both components together ($ewsum$):

$$\begin{aligned} ewsum_d &= \sum_{i=1}^{NT-1} delta_d[i] \times \mathrm{abs}(ewst_d[i]) \\ ewsum_m &= \sum_{i=1}^{NT-1} delta_m[i] \times \mathrm{abs}(ewst_m[i]) \end{aligned} \tag{5.2}$$

and

$$ewsum = ewsum_d + ewsum_m \ . \tag{5.3}$$

The variables $delta_d[i]$ and $delta_m[i]$ take only values 1 or 0 depending on considering or not considering the corresponding trait.

The following proportions of standardized economic weights (which are called relative economic weights) may be calculated:

- Standardized economic weight for the direct component of trait $i$ expressed as percentage of the sum of all standardized economic weights for the direct components:

$$ewr_dd[i] = 100 \times \frac{\text{abs}(ewst_d[i])}{ewsum_d} \tag{5.4}$$

- Standardized economic weight for the direct component of trait $i$ expressed as percentage of the sum of all standardized economic weights for both the direct and the maternal components:

$$ewr_da[i] = 100 \times \frac{\text{abs}(ewst_d[i])}{ewsum} \tag{5.5}$$

- Standardized economic weight for the maternal component of trait $i$ expressed as percentage of the sum of all standardized economic weights for the maternal components:

$$ewr_mm[i] = 100 \times \frac{\text{abs}(ewst_m[i])}{ewsum_m} \tag{5.6}$$

- Standardized economic weight for the maternal component of trait $i$ expressed as percentage of the sum of all standardized economic weights for both the direct and the maternal components:

$$ewr_ma[i] = 100 \times \frac{\text{abs}(ewst_m[i])}{ewsum} \tag{5.7}$$

# Chapter 6

# Installing and running the program

## 6.1 List of files in the installation package

The program GFSH is distributed together with the program EWSH2 [6]. Therefore, files for both programs are in the installation package. The files are in five directories.

### 6.1.1 Directory PROG

This directory contains executable program files and text files which are not to be edited.

**ewsh2.exe** Executable file for program EWSH2 [6].

**gfsh.exe** Executable file for program GFSH.

**TEXTS2_OUT.TXT** This file contains text for writing the results for the program EWSH2. For further details see the manual for the program EWSH2 [6].

**TEXTGFS_OUT.TXT** This file contains text for writing the results for the program GFSH. See also Section 7.3.

**P01_00.TXT** This file contains the initial parameters for the production system ($prods = 1$), the breed ($breed = 1$) and the number of the run of EWSH2 ($calc = 1$) for production system 1.

**P02_00.TXT** This file contains the initial parameters for the production system ($prods = 2$), the breed ($breed = 2$) and the number of the run of EWSH2 ($calc = 1$) for production system 2.

**ERROR.TXT** A text file forwarding error messages between succesive runs of the program EWSH2 and the program GFSH. The file in this directory contains the starting value 0 which means no error message.

**cygwin1.dll** This is a file from Cygwin which is necessary for running the programs under Windows. It is contained only in the distribution for Windows.

### 6.1.2 Directory PS1

This directory contains files necessary for running production system 1. Production system 1 is only for one breed. Without loss of generality, we will call this breed A.

**PARASA.TXT** Parameter file which contains the most important parameters for running the program EWSH2. For further details see the manual for the program EWSH2 [6].

**PARAGFS.TXT** Parameter file which contains the most important parameters for running the program GFSH (see Section 7.1.2).

**INPUTS#A.TXT with # = 01, 02, ..., 14** Data input files for program EWSH2. Not all data input files are needed for all calculations. For further details see the manual for the program EWSH2 [6].

**INPUTGFS#.TXT with # = 01A, 02, 04** Data input files for program GFSH (see Section 7.2).

**ps1A.sh under LINUX or ps1A.bat under Windows** This is the shell script (LINUX) or batch file (Windows) which starts the calculations for production system 1.

### 6.1.3 Directory PS2

This directory contains files necessary for running production system 2. This is a system with terminal crossing. There are two breeds. Breed A is the sire breed and breed B is the dam breed.

**PARASA.TXT, PARASB.TXT** Parameter files for breeds A and B, respectively, which contain the most important parameters for running the program EWSH2 for the given breed. For further details see the manual for the program EWSH2 [6].

**PARAGFS.TXT** Parameter file which contains the most important parameters for running the program GFSH (see Section 7.1.2).

**INPUTS#A.TXT and INPUTS#B.TXT with # = 01, 02, ..., 14** Data input files for breeds A and B, respectively, for program EWSH2. Not all data input files are needed for all calculations. For further details see the manual for the program EWSH2 [6].

**INPUTGFS#.TXT with # = 01A, 01B, 03, 04** Data input files for program GFSH (see Section 7.2).

**ps2AB.sh under LINUX or ps2AB.bat under Windows** This is the shell script (LINUX) or batch file (Windows) which starts the calculations for production system 2.

### 6.1.4 Directory DOC

**license** This file contains the license conditions. Read them carefully and do not use the program package ECOWEIGHT if you do not agree with the license conditions.

**ECOWEIGHT03A.pdf** Part 3A of the documentation of the program package ECOWEIGHT, manual for the program EWSH2.

**ECOWEIGHT03B.pdf** Part 3B of the documentation of the program package ECOWEIGHT, manual for the program GFSH.

### 6.1.5 Directory SRC

This directory contains the source files in C language.

**ewsh2.c** Source code of the program EWSH2.

**gfsh.c** Source code of the program GFSH.

## 6.2 Installation

### 6.2.1 Under LINUX

The program GFSH together with the program EWSH2 come to you as a compressed tar-file with the name ECOWEIGHT03_{# of version}.tgz, for example ECOWEIGHT03_5_0_2.tgz contains the programs from version 5.0.2 of the program package. Copy this file to a directory of your choice and enter the command

tar xvf ECOWEIGHT03_{# of version}.tgz

for uncompressing and unarchiving the file. You will get the file structure as described in Section 6.1.

**Only for experts in programming.** If you want to do changes in the program (source code) by yourself, then you must use the option -lm for compiling the source code when using the compiler gcc because otherwise the mathematical functions would not work; e.g.

gcc -lm -o gfsh.exe gfsh.c

will compile the source file gfsh.c to the executable file gfsh.exe.

### 6.2.2 Under Microsoft Windows

The Windows version of the program is distributed as zip file with the name ECOWEIGHT03_{# of version}.zip. It contains the compiled programs *ewsh2.exe* and *gfsh.exe*. The programs were compiled under Cygwin (http:// www.cygwin.com) and run only in the presence of the file *cygwin1.dll* which is part of the Windows distribution.

**Only for experts in programming.** If you intend to change the source code and to compile the program you are recommended to install Cygwin which is freely available. When compiling the source code, the following statement works for the program EWSH2:

gcc -Wl,–stack=55000000 -o ewsh2.exe ewsh2.c

The program GFSH can be simply compiled by the statement

gcc -o gfsh.exe gfsh1.c

Alternatively it should be possible to use commercial C compilers (we did not test commercial compilers).

## 6.3 Running the program

You are recommended to create one directory for each calculation where you will copy and edit all files you will need. The program may be also in this directory or may be copied to a directory for executable files, e.g. to the directory /usr/local/bin in LINUX.

### 6.3.1 Running the program for production system 1

All files needed for running production system 1 are in the directory PS1. Furthermore, the directory PROG is needed where the program files and further files are located which should not be edited. The directories PS2, DOC and SRC are not needed for the calculation.

Edit the parameter files PARASA.TXT and PARAGFS.TXT and the input files INPUTS#A.TXT with # = 01, 02, ..., 14 and INPUTGFS#.TXT with # = 01A, 02, 04 in directory PS1. Under LINUX, type *./ps1A.sh* and press ENTER to start the shell script which runs the programs EWSH2 and GFSH. Under Windows, type *ps1A.bat* and press ENTER to start the batch file which runs the programs EWSH2 and GFSH.

For redirecting the text written to the screen to a text file, say a.txt, type *./ps1A.sh* > *a.txt* under LINUX or *ps1A.bat* > *a.txt* under Windows and press ENTER.

The shell script *ps1A.sh* for running production system 1 looks like that:

```
#!/bin/sh
echo '********************************'
echo I am copying P01_00.TXT to P00.TXT
echo '********************************'
cp ../PROG/P01_00.TXT P00.TXT
echo ' '
echo '************************************************'
echo 'I am copying TEXT*_OUT.TXT to the working directory'
echo '************************************************'
cp ../PROG/TEXTS2_OUT.TXT .
cp ../PROG/TEXTGFS_OUT.TXT .
echo ' '
echo '******************************************'
echo 'I am copying ERROR.TXT to the working directory'
echo '******************************************'
cp ../PROG/ERROR.TXT .
echo ' '
echo '*************************'
echo I am starting program EWSH2
echo '*************************'
./../PROG/ewsh2.exe
echo ' '
echo '*************************'
echo I am starting program GFSH
echo '*************************'
```

```
./../PROG/gfsh.exe
echo ' '
echo '**********'
echo I am ready
echo '**********'
```

The following two results files will printed:

- *resA01*: This is the results file from program EWSH2.
- *resgfps01*: This is the results file from program GFSH described in this manual.

Furthermore, the values of all variables are printed for both programs in the following files:

- *CHECKSA01*: Complete list of the values of all variables of breed A from program EWSH2 at the end of the calculation. The description of the variables is given in Appendix B in the manual for EWSH2 [6].
- *CHECKSA01a*: Complete list of the values of all variables of breed A from program EWSH2 before the program starts the calculation of economic values. This file is printed mainly as help for further programming and as a check for correct computing. With one exception (variable $zr$, number of the loop), the values of all variables contained in both files must be equal. The file CHECKSA01a does not contain the economic values which are printed only in CHECKSA01.
- *CHECKGFS*: Complete list of the values of all variables from program GFSH. The description of the variables is given in Appendix B of the present manual.

### 6.3.2 Running the program for production system 2

All files needed for running production system 2 are in the directory PS2. Furthermore, the directory PROG is needed where the program files and further files are located which should not be edited. The directories PS1, DOC and SRC are not needed for the calculation.

Edit the parameter files PARASA.TXT, PARASB.TXT and PARAGFS.TXT and the input files INPUTS#A.TXT with # = 01, 02, ..., 14, INPUTS#B.TXT with # = 01, 02, ..., 14 and INPUTGFS#.TXT with # = 01A, 01B, 03, 04 in directory PS2. Under LINUX, type *./ps2AB.sh* and press ENTER to start the shell script which runs several times the program EWSH2 and then the program GFSH. Under Windows, type *ps2AB.bat* and press ENTER to start the batch file which runs the programs EWSH2 and GFSH.

For redirecting the text written to the screen to a text file, say a.txt, type *./ps2AB.sh* > *a.txt* under LINUX or *ps2AB.bat* > *a.txt* under Windows and press ENTER.

The shell script *ps2AB.sh* for running production system 2 has the following structure:

```
#!/bin/sh
echo '********************************'
echo I am copying P02_00.TXT to P00.TXT
echo '********************************'
cp ../PROG/P02_00.TXT P00.TXT
echo ' '
```

```
echo '************************************************'
echo 'I am copying TEXT*_OUT.TXT to the working directory'
echo '************************************************'
cp ../PROG/TEXTS2_OUT.TXT .
cp ../PROG/TEXTGFS_OUT.TXT .
echo ' '
echo '******************************************'
echo 'I am copying ERROR.TXT to the working directory'
echo '******************************************'
cp ../PROG/ERROR.TXT .
echo ' '
echo '*********************************'
echo I am starting program EWSH2, breed B
echo '*********************************'
./../PROG/ewsh2.exe
echo ' '
echo '*********************************'
echo I am starting program EWSH2, breed A
echo '*********************************'
./../PROG/ewsh2.exe
echo ' '
echo '*********************************'
echo I am starting program EWSH2, breed A
echo '*********************************'
./../PROG/ewsh2.exe
echo ' '
echo '*********************************'
echo I am starting program EWSH2, breed B
echo '*********************************'
./../PROG/ewsh2.exe
echo ' '
echo '************************'
echo I am starting program GFSH
echo '************************'
./../PROG/gfsh.exe
echo ' '
echo '**********'
echo I am ready
echo '**********'
```

The following results files will printed:

- *resB01*: This is the results file from the first run of program EWSH2 which is for breed B.
- *resA02*: This is the results file from the second run of program EWSH2 which is for breed A.
- *resA03*[1]: This is the results file from the third run of program EWSH2 which is for breed A.
- *resB04*[2]: This is the results file from the forth run of program EWSH2 which

[1] This file contains the final results for breed A from the program EWSH as the third run of EWSH is the last run for breed A.

[2] This file contains the final results for breed B from the program EWSH2 as the forth run of EWSH2 is the last run for breed B.

is for breed B.

- *resgfps02*: This is the results file from program GFSH described in this manual.

Furthermore, the values of all variables are printed for both programs in the following files:

- *CHECKSB01*: Complete list of the values of all variables of breed B from the first run of program EWSH2 at the end of the calculation. The description of the variables is given in Appendix B in the manual for EWSH2 [6].
- *CHECKSB01a*: Complete list of the values of all variables of breed B from the first run of program EWSH2 before the program starts the calculation of economic values. This file is printed mainly as help for further programming and as a check for correct computing. With one exception (variable $zr$, number of the loop), the values of all variables contained in both files must be equal. The file CHECKSB01a does not contain the economic values which are printed only in CHECKSB01.
- *CHECKSA02*: Complete list of the values of all variables of breed A from the second run of program EWSH2 at the end of the calculation.
- *CHECKSA02a*: Complete list of the values of all variables of breed A from the second run of program EWSH2 before the program starts the calculation of economic values.
- *CHECKSA03*[3]: Complete list of the values of all variables of breed A from the third run of program EWSH2 at the end of the calculation.
- *CHECKSA03a*: Complete list of the values of all variables of breed A from the third run of program EWSH2 before the program starts the calculation of economic values.
- *CHECKSB04*[4]: Complete list of the values of all variables of breed B from the forth run of program EWSH2 at the end of the calculation.
- *CHECKSB04a*: Complete list of the values of all variables of breed B from the forth run of program EWSH2 before the program starts the calculation of economic values.
- *CHECKGFS*: Complete list of the values of all variables from program GFSH. The description of the variables is given in Appendix B of the present manual.

## 6.4 General remarks

Several checks of input parameters are included in the programs. For example, certain input parameters have to sum to one. A warning will appear if these input parameters are invalid and the program will stop. You will be told which input parameters to correct before restarting the program. In general, it is your responsibility to use input parameters which are realistic and fit together, because it is impossible to predict any possible erroneous combinations of input parameters. Do not forget to have always a critical look on your results before using them for further purposes.

[3] See footnote 1 on the previous page.
[4] See footnote 2 on the preceding page.

# Chapter 7

# Input files

**Important remark:** When editing the input files, keep attention *not to change quotation marks*. All files are read as sequential files and the program recognizes the beginning and the end of texts on the basis of quotation marks. Adding or deleting a quotation mark will cause the program to break down or to calculate wrong results.

**Monetary unit:** In all input files the abbreviation MU is used for monetary unit. All values in the distributed version of the program refer to Euros. You can globally replace the abbreviation MU by the abbreviation of your monetary unit in all data input files (INPUTGFS#.TXT) with # = 01A, 01B, 02, 03, 04 and in the input file TEXTGFS_OUT.TXT (which is located in the directory PROG) using any text editor; the results file(s) will then contain the monetary unit specified by you.

**Language of the program:** The program will need just the numbers for calculations. The texts are read in and printed out to the result file as they are. Therefore, you can freely change the text in all input files as long as you do not modify the quotation marks. For example, you can translate all texts in the input files to another language what will cause the appropriate part of the result file to be printed in the same language as the input files (may be there are some exceptions where the English text will be remained). The length of the texts can be changed, but each text must start and finish with quotation marks. A great part of the text for the results file(s) is read from the file TEXTGFS_OUT.TXT (which is located in the directory PROG). You can translate all the text in this file. But be very careful not to change quotation marks.

## 7.1 Parameter files

### 7.1.1 File P01.TXT

The file P01.TXT is generated by the program EWSH2 and contains only one number - the code for the production system (*prods*). This code is

- 1 for a pure-bred system of breed A with one production level
- 2 for a production system with breeds A and B, each on one production level; partially terminal crossing is applied

### 7.1.2 File PARAGFS.TXT

This file contains basic information for running the program GFSH. At the beginning of the file between the first two quation marks you can write any text characterizing your calculation. Then the value of a parameter is always followed by its description. Modify the values of the parameter(s) according to your needs. In the recent version of the program, the file contains only one parameter:

- Genetic standard deviations for the direct and maternal components of the traits
  - 1: are not known or are not intended to be used for the calculation of relative economic weights
  - 2: are known and given in INPUTGFS04.TXT

## 7.2 Data input files

### 7.2.1 Input file INPUTGFS01A.TXT

This file is produced by the program EWSH2 and should not be edited. It contains the following input values for breed A (only numbers, no text):

- Annual discount rate ($u$)
- Number of breeding cycles for rams of breed A ($RRA$)
- Proportion of rams of breed A entering each breeding cycle ($l4RA[i]$)
- Number of reproductive cycles for ewes of breed A($LLA$)
- Proportion of ewes of breed A entering each reproductive cycle ($l4EA[i]$)
- Marginal economic values for all traits of breed A in the unit as they are printed ($evpA[i][1]$) by the program EWSH2. The value 0.000000 is inserted for economic values which were not calculated in the given system.
- Age of rams of breed A used for pure-breeding at the beginning of the first breeding cycle ($ageR11A$)
- Age of ewes of breed A at first lambing ($ageE1A$)

### 7.2.2 Input file INPUTGFS01B.TXT

This file is produced by the program EWSH2 and should not be edited. It is not read for production system 1. It contains the following input values for breed B (only numbers, no text):

- Number of breeding cycles for rams of breed B ($RRB$)
- Proportion of rams of breed B entering each breeding cycle ($l4RB[i]$)
- Number of reproductive cycles for ewes of breed B ($LLB$)
- Proportion of ewes entering each reproductive cycle ($l4EB[i]$)
- Marginal economic values for all traits expressed in pure-bred animals of breed B ($j = 1$) or in cross-bred animals A×B ($j = 2$) in the unit as they are printed in the program EWSH2 ($evpB[i][j]$). The values for all traits of pure-bred animals are given first followed by the values for cross-bred animals. The value 0.000000 is inserted for economic values which were not calculated in the given system.

- Age of rams of breed B at the beginning of the first breeding cycle ($ageR11B$)
- Age of rams of breed A used for crossing with ewes of breed B at the beginning of the first breeding cycle ($ageR12A$)
- Age of ewes of breed B at first lambing ($ageE1B$)
- Fraction of ewes of breed B crossed with rams of breed A for reproductive cycles $i = 0, \ldots, LLB - 1$. $pcrossE[0]$ is the fraction of female lambs crossed.

### 7.2.3 Input file INPUTGFS02.TXT

This file contains input parameters for calculating the transmission matrix **P** for gene flow for production system 1 (pure-bred system with one production level). When filling in the numbers you must know the number of age classes for sires and dams which you can easily calculate from equations (3.1) and (3.2). For example, assume that the age of rams at the beginning of the first breeding cycle is 580 days. Dividing this age by 365 you get the age in years which is 1.59. Applying the function int (integer) which truncates the decimal portion of the value of the argument you get the value 1. Assume that the number of breeding cycles is 5. Then you get 6 age classes for sires as result. In the first age class there are animals with an age up to 1 year, in the second class animal with an age up to 2 years etc.

The following values are read from the input file:

- Number of sex and age class for which the gene flow will be calculated ($n_sac$)
- Length of the investment period ($l_inv$)
- Indicator variable #1 ($pgssA$). Insert 1, if the proportion of genes from the individual age classes of sires in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of sires in male progeny are automatically inserted by the program, i.e. equal proportions as in the ram flock are assumed.
- Indicator variable #2 ($pgdsA$). Insert 1, if the proportion of genes from the individual age classes of dams in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of dams in male progeny are automatically inserted by the program, i.e. equal proportions as in the ewe flock are assumed.
- Proportions of genes from individual age classes of sires in male progeny (path sires to sires, the numbers must sum to 0.5, $P[1][1]$ to $P[1][acsA]$). These values are only read if indicator variable #1 is set to 1.
- Proportions of genes from individual age classes of dams in male progeny (path dams to sires, the numbers must sum to 0.5, $P[1][acsA + 1]$ to $P[1][acsA + acdA]$). These values are only read if indicator variable #2 is set to 1.

### 7.2.4 Input file INPUTGFS03.TXT

This file contains input parameters for calculating the transmission matrix **P** for gene flow for production system 2 (cross-bred system with two breeds on one production level applying partly terminal crossing). The file has a similar structure as INPUTGFS02.TXT. When filling in the numbers you must know the number of sex and age classes which can be calculated as shown at the beginning of Chapter 4. See also the explanations to input file INPUTGFS02.TXT.

The following values are read from the input file:

- Proportion of ewes of breed A in the production system ($pdA$)
- Proportion of ewes of breed B in the production system ($pdB$)
- Number of the sex and age class for which the gene flow will be calculated ($n_sac$)
- Length of the investment period ($l_inv$)
- Indicator variable #1 ($pgssA$). Insert 1, if the proportion of genes from the individual age classes of sires of breed A in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of sires of breed A in male progeny are automatically inserted by the program, i.e. equal proportions as in the ram flock are assumed.
- Indicator variable #2 ($pgdsA$). Insert 1, if the proportion of genes from the individual age classes of dams of breed A in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of dams of breed A in male progeny are automatically inserted by the program, i.e. equal proportions as in the ewe flock are assumed.
- Indicator variable #3 ($pgssB$). Insert 1, if the proportion of genes from the individual age classes of sires of breed B in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of sires of breed B in male progeny are automatically inserted by the program, i.e. equal proportions as in the ram flock are assumed.
- Indicator variable #4 ($pgdsB$). Insert 1, if the proportion of genes from the individual age classes of dams of breed B in male progeny are to be read from this file and insert 2, if the proportion of genes from the individual age classes of dams of breed B in male progeny are automatically inserted by the program, i.e. equal proportions as in the ewe flock are assumed.
- Proportions of genes from individual age classes of sires of breed A in male progeny A (path sires A to sires A, the numbers must sum to 0.5, $P[1][1]$ to $P[1][acsA]$). These values are only read if indicator variable #1 is set to 1.
- Proportions of genes from individual age classes of dams of breed A in male progeny A (path dams A to sires A, the numbers must sum to 0.5, $P[1][acsA+1]$ to $P[1][acsA + acdA]$). These values are only read if indicator variable #2 is set to 1.
- Proportions of genes from individual age classes of sires of breed B in male progeny B (path sires B to sires B, the numbers must sum to 0.5, $P[acsA + acdA + acsAB + 1][acsA + acdA + acsAB + 1]$ to $P[acsA + acdA + acsAB + 1][acsA + acdA + acsAB + acsB]$). These values are only read if indicator variable #3 is set to 1.
- Proportions of genes from individual age classes of dams of breed B in male progeny B (path dams B to sires B, the numbers must sum to 0.5, $P[acsA + acdA + acsAB + 1][acsA + acdA + acsAB + acsB + 1]$ to $P[acsA + acdA + acsAB + 1][acsA + acdA + acsAB + acsB + acdB]$). These values are only read if indicator variable #4 is set to 1.

### 7.2.5 Input file INPUTGFS04.TXT

This input file contains the genetic standard deviations for calculating the relative economic weights for direct and maternal components of all traits. Keep attention that the units of the genetic standard deviations are the same as the units of the economic weights (the units given in this file). The genetic standard deviations must be for the breed the economic weights are calculated for. The appropriate input is skipped if the trait is not considered in the calculation.

Genetic standard deviations for both direct and maternal components of the traits are read for traits 1 to 3, 21, 23 and 24 (see Appendix A), genetic standard deviations are read only for the direct component in traits 4 to 7, 9 to 20 and 25 and for traits 8, 22 and 26 to 35 the genetic standard deviation is read only for the maternal component of the trait.

### 7.2.6 Input file INPUTGFS05.TXT

This file is important for the calculation of relative economic weigts. It is read only if the genetic standard deviations of the traits are known. In this file, you are asked to choose between two alternative definitions of the same trait. The two definitions are presented with the number of the traits (as given in Appendix A) in parantheses. Type the number of the definition you prefer. The appropriate input is skipped if the trait is not considered in the calculation. The following selections are to be made (the variable to which the numbers are read is given in parentheses):

- Select (2) weaning weight or (3) average daily gain from birth till weaning ($flag[1]$)
- Select (4) weight at the end of artificial rearing or (5) average daily gain in artificial rearing ($flag[2]$)
- Select (26) productive lifetime of ewes in reproductive cycles or (27) productive lifetime of ewes in years ($flag[3]$)
- Select (28) total milk yied in the standardized milking period or (29) average daily milk yield ($flag[4]$)
- Select (30) fat content in milk or (31) fat yield in the standardized milking period ($flag[5]$)
- Select (32) protein content in milk or (33) protein yield in the standardized milking period ($flag[6]$)

## 7.3 TEXTGFS_OUT.TXT

This file contains texts which are used for printing the results. It contains headings of sections of the results files, comments and names of variables the values of which are printed in the results files. For editing the file read carefully the remarks at the beginning of Chapter 7 on page 29.

## 7.4 ERROR.TXT

This file contains only the value of the variable *errmess*. At the start of each calculation of the program EWSH2 this file is read with the value 0 for *errmess*. If there occurs an error during the calculation of the program EWSH2, the value of *errmess* is changed to 1 and written to the file ERROR.TXT. In the next run of

EWSH2 or in the run of the program GFSH, the file ERROR.TXT is read again. If $errmess = 1$, all subsequent programs including GFSH will stop and write an error message.

# Chapter 8

# Program output

## 8.1 The results file

The name of the file the results are written to is fixed to *resgfps#* where # = 01 for production system 1 and # = 02 for production system 2. The first part of the file contains information on the version of the program, copyright and contact to the authors and the values of the system variables read from P01.TXT and PARAGFS.TXT (see Section 7.1.2). The second part of the file copies more or less the data input files INPUTGFS#.TXT where # is to be replaced by the corresponding numbers (see Section 7.2). The information read from the input files is selected according to the parameters given in the parameter file. Therefore, the results file does not contain a simple copy of the input files, but only data from input files which will be needed for the given calculation.

The third part of the results file contains the results in the following order:

- Number of the production system
- Number of the sex and age class the cumulative number of discounted expressions and the economic weights are calculated for
- Cumulative number of discounted expressions in all sex and age classes at the end of the investment period (vector $m_sum[*]$)
- Length of the investment period
- Economic weights for direct and maternal components of the individual traits expressed in monetary units per unit of trait and per ewe in the whole breeding system
- Economic weights per genetic standard deviation for direct and maternal components of the individual traits and per ewe in the whole breeding system
- Relative economic weights
  - Standardized economic weights for direct or maternal trait components as percentage of the sum of absolute values of standardized economic values for direct or maternal trait components, respectively
  - Standardized economic weights for direct or maternal trait components as percentage of the sum of absolute values of standardized economic values for both direct or maternal trait components

**Remark.** A dense network of conditions was used in the program to ensure printing out only the items relevant for the given production systems. But it cannot fully be guaranteed that no variables not meaningful for the given calculation slipped through the meshes. In these cases don't worry, as the values of these variables are (hopefully) ignored in the calculation.

## 8.2 File CHECKGFS

The file CHECKGFS is mainly thought as a help in programming. The file contains only the names and the values of all variables in alphabetic order without further explaining text. The names of all variables are given in Appendix B.

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# Appendix A

# Numbering of traits in the program

1. Birth weight
2. Weaning weight. The economic weight is calculated only if there is customary weaning.
3. Average daily gain from birth until weaning. The economic weight is calculated only if there is customary weaning.
4. Weight at the end of artificial rearing. The economic weight is calculated only if there is artificial rearing.
5. Average daily gain in artificial rearing. The economic weight is calculated only if there is artificial rearing.
6. Average daily gain of breeding animals during rearing
7. Average daily gain in fattening. The economic weight is calculated only if there is fattening.
8. Mature weight
9. Dressing percentage of lambs at weaning or at the end of artificial rearing. The economic weight is calculated only if there is a pricing system where dressing percentage is paid for.
10. Dressing percentage of fattened lambs. The economic weight is calculated only if there is fattening and if there is a pricing system where dressing percentage is paid for.
11. Dressing percentage of adult sheep. The economic weight is calculated only if there is a pricing system where dressing percentage is paid for.
12. Average quality class for lambs at weaning or at the end of artificial rearing when paid for live weight. The economic weight is calculated only if animals are paid for live weight.
13. Average quality class for fattened lambs when paid for live weight. The economic weight is calculated only if animals are paid for live weight.
14. Average quality class for adult sheep when paid for live weight. The economic weight is calculated only if animals are paid for live weight.

15. Average class for fleshiness for adult sheep. The economic weight is calculated only if animals are paid for carcass quality.

16. Average class for fat covering for adult sheep. The economic weight is calculated only if animals are paid for carcass quality.

17. Average class for fleshiness for fattened lambs and/or for heavy lambs (carcass weight $>$ 13 kg) slaughtered after weaning or after artificial rearing. The economic weight is calculated only if animals are paid for carcass quality. Lambs slaughtered after weaning are included only for non-dairy breeds.

18. Average class for fat covering for fattened lambs and/or for heavy lambs (carcass weight $>$ 13 kg) slaughtered after weaning or after artificial rearing. The economic weight is calculated only if animals are paid for carcass quality. Lambs slaughtered after weaning are included only for non-dairy breeds.

19. Average class for carcass quality for lambs slaughtered after weaning or artificial rearing. The economic weight is calculated only if animals are paid for carcass quality.

20. Conception rate of female lambs

21. Average conception rate of ewes

22. Average litter size for lambing ewes

23. Average survival rate of lambs at lambing

24. Average survival rate of lambs till weaning. The economic weight is calculated only if there is customary weaning.

25. Average survival rate of lambs till the end of artificial rearing. The economic weight is calculated only if there is artificial rearing.

26. Average productive lifetime of ewes in numbers of reproductive cycles

27. Average productive lifetime of ewes in years

28. Total milk yield in the standardized milking period

29. Average daily milk yield for the whole milking period

30. Fat content in milk

31. Milk fat yield in the standardized milking period

32. Protein content in milk

33. Milk protein yield in the standardized milking period

34. Somatic cell score

35. Fleece weight

# Appendix B

# List of variables and constants

This list contains all variables used in the program. Some additional variables which are used only in the manual as they are useful for a clear arrangement and which are explained there are not part of the list.

| | |
|---|---|
| a2 | Temporary variable |
| a3 | Temporary variable |
| acdA | Number of age classes for dams in breed A |
| acdB | Number of age classes for dams in breed B |
| ACM | Maximal dimension of the transmission matrix for gene flow |
| acm | Dimension of the transmission matrix for gene flow |
| acsA | Number of age classes for sires of breed A used for pure-breeding |
| acsAB | Number of age classes for sires of breed A used for cross-breeding with ewes of breed B |
| acsB | Number of age classes for sires of breed B used for pure-breeding |
| ageE1A | Age of ewes of breed A at the first lambing |
| ageE1B | Age of ewes of breed B at the first lambing |
| ageR11A | Age of rams of breed A used for pure-breeding at the beginning of the first breeding cycle |
| ageR11B | Age of rams of breed B at the beginning of the first breeding cycle |
| ageR12A | Age of rams of breed A used for crossing with ewes of breed B at the beginning of the first breeding cycle |
| CB | Differentiates between cross-breeding and pure-breeding (set to 3, used for dimensioning arrays in the program) |
| delta_d[i] | Variable which indicates if the relative economic weight for the direct component of trait $i$ is calculated ($delta_d[i] = 1$) or not ($delta_d[i] = 0$) |
| delta_m[i] | Variable which indicates if the relative economic weight for the maternal component of trait $i$ is calculated ($delta_m[i] = 1$) or not ($delta_m[i] = 0$) |

errmess Variable indicating the presence ($errmess = 1$) or the absence ($errmess = 0$) of an error during the calculation when running EWSH2. The value of this variable is forwarded to the next run of EWSH2 and to GFSH and causes the following calculations to stop if an error occurred in one of the preceding programs.

evpA[i][1] Marginal economic value of trait $i$ expressed in pure-bred animals of breed A with units used for printing the results in the program EWSH2

evpB[i][j] Marginal economic value of trait $i$ expressed in pure-bred ($j = 1$) or cross-bred ($j = 2$) animals of breed B with units used for printing the results in the program EWSH2

ew_d[i] Economic weight for the direct effect of trait $i$

ew_m[i] Economic weight for the maternal effect of trait $i$

ewr_da[i] Standardized economic weight for the direct component of trait $i$ expressed as percentage of the sum of all standardized economic weights for both the direct and the maternal components (see equation 5.5)

ewr_dd[i] Standardized economic weight for the direct component of trait $i$ expressed as percentage of the sum of all standardized economic weights for the direct components (see equation 5.4)

ewr_ma[i] Standardized economic weight for the maternal component of trait $i$ expressed as percentage of the sum of all standardized economic weights for both the direct and the maternal components (see equation 5.7)

ewr_mm[i] Standardized economic weight for the maternal component of trait $i$ expressed as percentage of the sum of all standardized economic weights for the maternal components (see equation 5.6)

ewst_d[i] Standardized economic weight for the direct component of trait $i$ (see equation 5.1)

ewst_m[i] Standardized economic weight for the maternal component of trait $i$ (see equation 5.1)

ewsum Sum of the absolute values of the standardized economic weights for both the direct and the maternal trait components ($ewsum_d + ewsum_m$)

ewsum_d Sum of the absolute values of the standardized economic weights for the direct trait components (see equation 5.2)

ewsum_m Sum of the absolute values of the standardized economic weights for the maternal trait components (see equation 5.2)

flag[i] Chooses always between two trait definitions in the calculation of relative economic weights (see Table B.1).

gstd Indicator variable if the genetic standard deviations for the direct and maternal components of the traits are not known or are not intended to be used for the calculation of relative economic weights ($gstd = 1$) or are known and given in INPUTGFS04.TXT ($gstd = 2$)

gstd_d[i] Genetic standard deviations for the direct component of trait $i$ ($i = 1, \ldots, NT - 1$)

Table B.1: Possible values of the variable $flag[i]$. The values of the variable correspond to the numbers of the trait definitions as given in Appendix A.

| Value of $i$ | Possible values of $flag[i]$ |
|---|---|
| 1 | 2, 3 |
| 2 | 4, 5 |
| 3 | 26, 27 |
| 4 | 28, 29 |
| 5 | 30, 31 |
| 6 | 32, 33 |

gstd_m[i] Genetic standard deviations for the maternal component of trait $i$ ($i = 1, \ldots, NT - 1$)

h_d[i] Realization vector $\mathbf{h_d}$ of dimension $acm$ for direct effects used in the calculation of gene flow (see Chapter 2)

h_m[i] Realization vector $\mathbf{h_m}$ of dimension $acm$ for maternal effects used in the calculation of gene flow (see Chapter 2)

he_d[i][j] Vector $\mathbf{h_d}$ multiplied with economic weights of trait $i$; $j$ is the sex and age class

he_m[i][j] Vector $\mathbf{h_m}$ multiplied with economic weights of trait $i$; $j$ is the sex and age class

i Index variable

j Index variable

L Maximal number of reproductive cycles + 1 (set to 16, used for dimensioning arrays in the program)

l_inv length of the investment period in years in time units (in years for production systems with one calving per year)

l4EA[i] Ewes of breed A entering reproductive cycle $i$ ($i = 1, \ldots, LLA$) expressed as proportion of ewes entering any reproductive cycle ( $\sum_{i=1}^{LLA} l4EA[i] = 1$)

l4EB[i] Ewes of breed B entering reproductive cycle $i$ ($i = 1, \ldots, LLB$) expressed as proportion of ewes entering any reproductive cycle ( $\sum_{i=1}^{LLB} l4EB[i] = 1$)

l4RA[i] Rams of breed A entering breeding cycle $i$ ($i = 1, \ldots, RRA$) expressed as proportion of rams entering any breeding cycle ( $\sum_{i=1}^{RRA} l4RA[i] = 1$)

l4RB[i] Rams of breed B entering breeding cycle $i$ ($i = 1, \ldots, RRB$) expressed as proportion of rams entering any breeding cycle ( $\sum_{i=1}^{RRB} l4RB[i] = 1$)

LLA Number of reproductive cycles for ewes of breed A

LLB Number of reproductive cycles for ewes of breed B

m_gf[i] Vector $\mathbf{m}$ of dimension $acm$ used in the calculation of gene flow (see Chapter 2); $i = 1, \ldots, acm$ is the sex and age class

m_gft[i] Vector $\mathbf{m}$ of dimension $acm$ used in the calculation of gene flow at the end of the investment period (see Chapter 2); $i$ is the sex and age class

m_sum[i] Vector $\sum_{t=1}^{l_inv} \mathbf{m}^{[\mathbf{t}]}(1+u)^{-t}$ of dimension $acm$ used in the calculation of gene flow (see Chapter 2). The vector contains the number of discounted expressions for the group of animals given by the variable $n_sac$ for the individual sex and age classes.

n2 Number of the input file

n3 Code for the use of capital letters in the name of the input file (0 = no letter, 1 = A, 2 = B etc.)

n_sac Number of the sex and age class for which the gene flow is calculated

NT Number of traits + 1

P[i][j] Gene transmission matrix $\mathbf{P}$ of dimension $acm \times acm$ for gene flow (see Chapter 2)

pcrossE[i] Fraction of ewes of breed B crossed with rams of breed A in reproductive cycle $i$ ($i = 1, \ldots, LL-1$). $pcrossE[0]$ is the fraction of female lambs crossed with breed A.

pdA Proportion of ewes of breed A in the production system

pdB Proportion of ewes of breed B in the production system

pgdsA Indicator variable for reading data. Insert 1, if the proportion of genes from the individual age classes of dams of breed A in male progeny are to be read from the file INPUTGFS02.TXT or INPUTGFS03.TXT and insert 2, if the proportion of genes from the individual age classes of dams of breed A in male progeny are automatically inserted by the program, i.e. equal proportions as in the ewe flock are assumed.

pgdsB Indicator variable for reading data. Insert 1, if the proportion of genes from the individual age classes of dams of breed B in male progeny are to be read from the file INPUTGFS03.TXT and insert 2, if the proportion of genes from the individual age classes of dams of breed B in male progeny are automatically inserted by the program, i.e. equal proportions as in the ewe flock are assumed.

pgssA Indicator variable for reading data. Insert 1, if the proportion of genes from the individual age classes of sires of breed A in male progeny are to be read from the file INPUTGFS02.TXT or INPUTGFS03.TXT and insert 2, if the proportion of genes from the individual age classes of sires of breed A in male progeny are automatically inserted by the program, i.e. equal proportions as in the ram flock are assumed.

pgssB Indicator variable for reading data. Insert 1, if the proportion of genes from the individual age classes of sires of breed B in male progeny are to be read from the file INPUTGFS03.TXT and insert 2, if the proportion of genes from the individual age classes of sires of breed B in male progeny are automatically inserted by the program, i.e. equal proportions as in the ram flock are assumed.

prods Production system; input parameter in the file P01.TXT (see Section 7.1.1 on page 29)

R Maximal number of breeding cycles for rams + 1 (set to 6, used for dimensioning arrays in the program)

| | |
|---|---|
| RRA | Number of breeding cycles for rams of breed A (input parameter) |
| RRB | Number of breeding cycles for rams of breed B (input parameter) |
| tt[i] | Type of trait: 0 for direct traits, 1 for maternal traits, 2 for traits with direct and maternal components; $i = 1, \ldots, NT - 1$ |
| u | Discount rate per time unit used in the gene flow method. The time unit is one year for production systems with one lambing per year. |
| zz | Variable used for numbering the input files in the results file |

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